

# Multi-trait selection of sweet sorghum (*Sorghum bicolor* (L.) Moench) genotypes for bioenergy production

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**Highlights:** The paper addresses the Bioenergy production and is important because sweet sorghum is a crop with high potential for bioenergy production

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**ABSTRACT** - The global demand for fuel from renewable sources has expanded rapidly in recent years and sweet sorghum is a crop with high potential for bioenergy production. This study aimed evaluate the performance of sweet sorghum hybrids belonging to the Embrapa Milho e Sorgo breeding program in different edaphoclimatic regions of Minas Gerais and to identify promising hybrids for bioenergy production, considering multiple traits of sweet sorghum. The study was conducted in two experimental areas of Embrapa Milho e Sorgo, in Sete Lagoas and Nova Porteirinha. A total of 36 sweet sorghum genotypes were evaluated, with 28 experimental hybrids and eight controls. The evaluated traits were: days from planting to flowering, plant height, fresh biomass yield, juice extraction, total soluble solids and tons of Brix per hectare. Analysis of variance, multiple comparison test, the Williams index of selection and the index suggested by Mulamba & Mock were performed. The results demonstrated the existence of genetic variability among the genotypes of sweet sorghum, demonstrating the possibility of selecting high-performance genotypes superior. The selection indexes employed were efficient in the selection of sweet sorghum hybrids with higher agroindustrial performance. It was possible to identify hybrids of sweet sorghum promising for bioenergy production.

**Keywords:** *Sorghum bicolor* (L.) Moench, hybrids, selection index.

## INTRODUCTION

The global demand for fuel from renewable sources has expanded rapidly in recent years due to concerns about reducing the volume of greenhouse gas emissions (Velmurugan et al., 2020; Appiah-Nkansah et al., 2019). Brazil has a tropical climate and high degree in agricultural technology, thus demonstrating a privileged position in relation other countries for the development and use of bioenergy crops (Taufiq-Yap et al., 2020).

Sweet sorghum (*Sorghum bicolor* (L.) Moench) is a crop with high potential for bioenergy production to complement sugarcane (Velmurugan et al., 2020; Appiah-Nkansah et al., 2019; Anandan et al., 2012). As sugarcane, sweet sorghum has a stem with high juice volume in fermentable sugars (Velmurugan et al., 2020; Naik et al., 2010; Ratnavathi et al., 2010). In addition, the short cycle (Rohowsky et al., 2013), the possibility of using the same equipment of sugarcane harvesting, milling and processing and the wide adaptability to different locals (Santos et al., 2015; Regassa & Wortmann, 2014).

The sweet sorghum hybrids are obtained from the cross between a male-sterile A (female) line with an R (restorative) line with dominant alleles for the fertility restoration gene (Smith and Frederiksen, 2000). Sweet sorghum hybrids should have favorable agronomic traits and provide quality feedstock that meet the technological demanded by the sugar and alcohol industry, for example, high stem yield capacity, lodging resistance, high percentage of extractable juice, a high total soluble solids content in the stem, resistance to major diseases, drought and flood tolerance, and tolerance to insecticides (Silva et al., 2017; Schaffert et al., 1980). However, these traits may modify throughout the development of the crop, such as the beginning of the accumulation of soluble solids in the stem from flowering to the physiological maturity, which may affect the recommendation of lines and hybrids for industrial planning (Andrade and Oliveira, 1988).

To perform simultaneous selection in plant breeding programs, one strategy is the use of selection indexes, which unites various information, resulting in a selection based on a set of variables, bringing together several traits of interest (Cruz, Regazzi, & Carneiro, 2012). When different selection criteria are considered, the gain prediction for each criterion is important to guide the breeder to select genetic material, maximizing the gain of interest (Rangel et al., 2011).

In view of the above, the objective was to identify and evaluate the performance of hybrids of sweet sorghum, belonging to the Embrapa Milho e Sorgo breeding program, promising for the production of bioenergy in edaphoclimatic regions of Minas Gerais.

## MATERIAL AND METHODS

The experiment was conducted in two experimental units of Embrapa Milho e Sorgo, in Sete Lagoas and in Nova Porteirinha, both municipalities located in the Minas Gerais state, in 2015/2016 crop year. Nova Porteirinha belongs to the northern region of the state of Minas Gerais, at latitude

15°45' S and longitude 43°17' W, typical climate is Aw (tropical with dry winter). The soil of the experimental area is characterized as medium-textured Red-Yellow Latosol. Sete Lagoas is located in the north-central part of the state of Minas Gerais at 19°28' S and 44°15' W, the typical climate is Aw, with dry winters and an average temperature in the coldest month greater than 18°C. The soil of the experimental area is characterized as textured Red-Yellow Latosol.

A total of 36 genotypes of sorghum were evaluated, as 28 experimental hybrids belonging to the Embrapa Milho e Sorgo breeding program (201555B001, 201555B002, 201555B003, 201555B004, 201555B005, 201555B006, 201555B007, 201555B008, 201555B009, 201555B010, 201555B011, 201555B012, 201555B013, 201555B014, 201555B015, 201555B016, 201555B017, 201555B018, 201555B019, 201555B020, 201555B021, 201555B022, 201555B023, 201555B024, 201555B025, 201555B026, 201555B027 and 201555B028) and eight controls that include four experimental varieties (CMSXS630, CMSXS643, CMSXS646, CMSXS647), two commercial varieties, (BRS 508 and BRS 511) and two commercial hybrids (CV198 and CV568). For obtaining the hybrids of sweet sorghum, ten male-sterile lines (A-lines) and five fertility restoration lines (R-lines) were used. These lines were crossed in a partial diallel scheme, in which the lines A, totaling 50 hybrids of sweet sorghum. F<sub>1</sub>'s seeds were obtained by manual crosses (in the field), in the experimental area of Embrapa Milho e Sorgo, located in the municipality of Sete Lagoas.

Each experimental plot consisted of two 5-m rows with 0.70 m between rows, totaling an area of 7.00 m<sup>2</sup>. The initial plant population used was 140,000 plants ha<sup>-1</sup>. Four hundred and fifty kilograms per hectare of 08:28:16 N-P-K formulation was applied in the row at planting, and 200 kg ha<sup>-1</sup> urea was applied side-dressed 25 d after planting. The control of weeds and pests and other agricultural practices were performed as recommended for sorghum cultivation in the region (Borém et al., 2014). Harvesting and data collection were made when the grains were in the maturity phase, ie phase of higher concentration of sugars in the stalk. The following traits were evaluated: days from planting to flowering (FLOW, days), which consists of the days between sowing and the pollen liberation of 50% of the plants in the plot; plant height (PH, m), measured from the soil surface to the top of the panicle; fresh biomass yield (FBY, t.ha<sup>-1</sup>), which was determined by weighing all plants in the useful plot; juice extraction (EXT, %), using a hydraulic press, from five to eight plants sampled randomly per plot, without panicles; total soluble solids (TSS, °Brix) and ton of brix per hectare (TBH, t.ha<sup>-1</sup>) was obtained by weighing two rows of each plot and converted to t.ha<sup>-1</sup>. The TBH measurement was determined by digital refractometer, where the reading is given directly in °Brix of the juice extracted from the stems. Ton of brix per hectare (TBH, t.ha<sup>-1</sup>) was calculated as follows:

$$TBH = FBY \times (TSS/100). \quad (1)$$

Each local was subject to analysis of variance, based on the plot mean for each evaluated trait, considering all effects, except for the experimental error, using the following statistical model:

$$Y_{ij} = \mu + B_j + G_i + e_{ij} \quad (2)$$

where:  $Y_{ij}$  is the observed phenotypic value of the  $i$ th genotype in the  $j$ th block;  $\mu$  is the overall mean;  $B_j$  is the effect of the  $j$ th block;  $G_i$  is the effect of the  $i$ th genotype;  $e_{ij}$  is the effect of experimental error.

Subsequently, a joint analysis of variance was performed for the two locals for all the traits evaluated, thus observing the interaction G x L, so that the genotype effect was considered as fixed and for the local the random effect, according to the following model:

$$Y_{ijk} = \mu + G_i + B/L_{jk} + L_k + GL_{ik} + e_{ijk}$$

where  $y_{ijk}$  is the phenotypic value observed for genotype  $i$  in block  $j$  and local  $k$ ;  $\mu$  is the general mean;  $G_i$  is the effect of genotype  $i$ , which was also divided into  $g_i$  and  $t_i$ , according to the individual analysis;  $B/L_{jk}$  is the fixed effect of block  $j$ , within the local  $k$  ( $j = 1, \dots, 3$ );  $L_k$  is the random effect of

the local  $k$  ( $k = (1, 2)$ );  $GL_{ik}$  is the effect of the interaction of genotype  $i$  with the local  $k$ ;  $e_{ijk}$  is the experimental error.

The multiple comparison procedure for all genotypes, in the two locals, was performed according to the Scott and Knott (1974) test at 5% probability. The Williams index (1962) and the index suggested by Mulamba & Mock (1978) were used to predict the genetic gains and to select superior individuals. According to the prioritization of the traits, different economic weights can be assigned for each trait. The economic weights assigned by trial were as follows: 1.5 for the TSS and FBY; 1.3 for the PH and TBH; and 1.1 for FLOW and EXT, according to the degree of importance established. Other economic weights were established from the experimental data, as recommended by Cruz (1990), using the coefficient of genetic variation ( $CV_g$ ) of the trait, the ratio between the coefficient of genetic variation and the experimental variation ( $CV_g/CV_e$ ) and the standard deviation (SD) of the trait. In addition, a graphical presentation was used to make it easier to visualize of the average performance of the hybrids selected. Data analysis was performed using the software Genes (Cruz, 2013).

## RESULTADOS E DISCUSSÃO

There was a significant difference ( $P < 0.01$ ) for the F test, among all the genotypes for all traits evaluated in both locals (Table 1). In addition, the effect of the hybrids and the controls was significant for the two locals for all traits. These results demonstrate the existence of genetic variability among the sweet sorghum genotypes evaluated, evidencing the possibility of selecting high-performance genotypes through the genetic improvement of sweet sorghum.

**Table 1.** Summary of individual analysis of variance for 36 sweet sorghum genotypes evaluated in Sete Lagoas and Nova Porteirinha.

Sete Lagoas							
Source of variation	DF	Mean square					
		FLOW	PH	FBY	EXT	TSS	TBH
Block	2	1.56	0.01	0.39	1.89	3.38	0.30
Genotypes (G)	35	58.80**	0.07**	263.52**	26.60**	1.64**	11.85**
Hybrids (H)	27	38.69**	0.05**	228.47**	21.45**	1.31**	12.84**
Controls (C)	7	48.94**	0.20**	289.93**	46.61**	2.90**	9.41*
H vs C	1	670.66**	0.00 <sup>ns</sup>	728.50**	25.81**	1.79*	2.17**
Error	70	2.68	0.01	1.25	1.36	0.35	0.93
General mean		79.87	3.10	53.46	60.52	18.52	9.86
Mean of hybrids		78.54	3.25	54.85	60.26	18.98	9.97
Mean of controls		84.54	3.09	48.60	61.44	18.27	9.09
$h^2$ (%)		93.05	63.29	99.47	93.65	73.12	92.35
CV(%)		2.28	4.39	2.01	1.92	3.20	9.81
Nova Porteirinha							
Source of variation	DF	Mean square					
		FLOW	PH	FBY	EXT	TSS	TBH
Block	2	28.36	0.00	3.21	5.71	1.80	2.76
Genotypes (G)	35	81.51**	0.21**	268.37**	41.43**	11.86**	11.99**
Hybrids (H)	27	17.83**	0.16**	245.05**	35.59**	11.95**	13.26**
Controls (C)	7	165.80**	0.33**	396.60**	65.52**	13.10**	3.97*
H vs C	1	1210.72*	0.52**	0.37 <sup>ns</sup>	30.49**	0.88 <sup>ns</sup>	33.64**
Error	70	4.61	0.02	1.10	1.67	0.94	1.36
General mean		68.86	3.16	69.90	29.30	18.48	12.76
Mean of hybrids		67.07	3.13	69.93	29.59	18.43	12.46
Mean of controls		75.12	3.30	69.79	28.31	18.65	13.80
$h^2$ (%)		74.10	86.63	99.54	95.28	92.12	89.71
CV(%)		3.12	4.70	1.50	4.41	5.25	9.15

\*\* , \* , ns: significant at 1%, 5% and not significant by the test of F. DF: degrees of freedom; FLOW: flowering; PH: plant height; FBY: fresh biomass production; EXT: juice extraction; TSS: total soluble solids; and TBH: tons of brix per hectare;  $h^2$ : heritability; CV: coefficient of variation.

Several studies have indicated wide variability in sweet sorghum genotypes, such as Elangovan et al. 2014. who studying 200 accessions of sweet sorghum found high variability among the genotypes for the main agroindustrial traits evaluated, such as variations in total soluble solids (9.35-20.82 %), reducing sugars (0.11-3.74 %), purity (49.33-80.72%), juice extraction/5 plants (1.42-1.67 mL), fresh stem weight/5 plants (1.67-6.25 g) and dry stem weight/5 plants (833 -5,000 g), sucrose concentration (7.2-15.5 %), sugar production (above 12 t.ha<sup>-1</sup>), and biomass production (36-140 t.ha<sup>-1</sup>).

The coefficient of variation (CV) ranged from 1.92% for EXT to 9.81% for TBH at Sete Lagoas and from 1.50% for FBY to 9.15% for TBH at Nova Porteirinha, indicating adequate experimental precision for the two locals. The hybrids performed better than the controls in Sete Lagoas for FLOW, PH, FBY, TSS and TBH traits, and in Nova Porteirinha the hybrids performed better for the traits PH, FBY and EXT. In addition, the genotypes evaluated in Nova Porteirinha flowered in a shorter period than in Sete Lagoas. According to Grenier et al. (2001), these variations in days to flower occur because sorghum cultivars respond differently to day length and temperature. These situations are justified since the accumulation of soluble solids in the stem starts at the beginning of flowering and extends until physiological maturity of the grain, in addition, the production of fresh biomass tends to diminish after the flowering (Tarpley and Vietor 2007; Almodares et al., 2007). According to the general mean, flowering occurred between 79 and 87 days in Sete Lagoas, and in Nova Porteirinha, with has mean temperatures, around 28° C, flowered between 68 and 86 days. However, it was observed that the hybrids flowered earlier than the controls in both locals. According to Rocha et al., (2018) and Reddy, Kumar & Reddy (2010) the hybrids when compared to the varieties, show better performance for some important traits in sweet sorghum cultivars such as yield, flowering and less sensitivity to photoperiod. According to Quinby & Karper (1945), this to be due to the action of complementary genes and it appears that the gene Ma "Maturity gene" is involved wherever extreme lateness occurs.

Fresh biomass yield (FBY) is a trait of great interest in the improvement of sweet sorghum because the fermentable sugars will be extracted from the stems. According to this variable, the mean production of the hybrids was 69.93 t.ha<sup>-1</sup> in Nova Porteirinha, being considerably higher than in Sete Lagoas (54.85 t.ha<sup>-1</sup>). Souza et al. (2013) when evaluating sweet sorghum varieties in different locals, also observed a great variation for the FBY values among the genotypes, ranging from 15.9 t ha<sup>-1</sup> to 65.14 t ha<sup>-1</sup>. In relation to heritability, the trait that presented the highest value in Sete Lagoas was FBY (99.47%), followed by EXT (93.65%) and TBH (92.35%). The highest heritability value at Nova Porteirinha was also for FBY (99.54%), followed by EXT (95.28%) and TSS (92.12%). The residuals showed normal distribution and homogeneity of variances, and the experiments could be evaluated together.

There was a significant effect ( $P \leq 0.01$ ) by the F test, among all genotypes for most of the traits, except FBY and TBH (Table 2). Regarding the local effects, there was a significant difference for most of the traits, with the exception of TSS. The interactions between hybrids x local and controls x local were significant for all traits evaluated ( $P \leq 0.01$ ).

Several studies on sweet sorghum have demonstrated interaction between genotype x local for traits related to yield of ethanol (Figueiredo et al., 2015, Bahadure et al., 2015, Elangovan et al., 2014; Makanda et al., 2012). Thus, genotypes evaluated in different locals may present different behavior in relation to local conditions and the study on the behavior of genotypes in different locals may aid in the recommendation of cultivars (Cruz, Regazzi & Carneiro, 2012). The coefficient of variation for the joint analysis varied from 1.76% for FBY to 9.48% for TBH and the ratio ( $CV_g/CV_e$ ) presented values greater than one for EXT and TSS traits, indicating satisfactory results for the selection of these traits (Cruz, Regazzi & Carneiro, 2012).

The multiple comparison procedure for all genotypes, in the two locals, for all the traits is shown in the Table 3.

**Table 2.** Summary of the joint analysis of variance for 36 sweet sorghum genotypes, evaluated in Sete Lagoas and Nova Porteirinha.

Source of variation	DF	Mean square					
		FLOW	PH	FBY	EXT	TSS	TBH
Block/local	4	14.96	0.01	1.80	3.80	2.59	1.53
Genotypes ( <i>G</i> )	35	97.43**	0.19*	313.91 <sup>ns</sup>	47.92**	9.24*	13.31 <sup>ns</sup>
Hybrids ( <i>H</i> )	27	30.76 <sup>ns</sup>	0.12 <sup>ns</sup>	242.90 <sup>ns</sup>	38.20*	9.63**	15.29 <sup>ns</sup>
Controls ( <i>C</i> )	7	105.42 <sup>ns</sup>	0.44*	380.92 <sup>ns</sup>	92.27*	9.05 <sup>ns</sup>	6.23 <sup>ns</sup>
<i>H vs C</i>	1	1841.79**	0.23 <sup>ns</sup>	486.85**	0.09 <sup>ns</sup>	0.07 <sup>ns</sup>	9.35 <sup>ns</sup>
Local ( <i>L</i> )	1	6556.01**	0.22**	14592.30**	52640.35**	0.085 <sup>ns</sup>	454.28**
<i>G x L</i>	35	43.87**	0.09**	217.93**	18.84**	4.26**	10.53**
<i>H x L</i>	27	25.77**	0.08**	241.60**	19.84**	3.62**	10.82**
<i>C x L</i>	7	109.32**	0.09**	108.29**	19.86**	6.95**	7.15**
<i>(H vs C) x L</i>	1	39.58**	0.29**	347.94**	56.20**	2.60*	26.45**
Error	140	3.65	0.02	1.18	1.51	0.65	1.15
General mean		74.37	3.13	61.68	44.91	18.50	11.31
Mean of hybrids		72.80	3.11	62.39	44.92	18.51	11.20
Mean of controls		79.83	3.19	59.19	44.87	18.46	11.70
$CV_e$ (%)		2.57	4.55	1.76	2.74	4.34	9.48
$CV_g$ (%)		1.25	2.69	0.74	3.99	5.40	7.69
$CV_g/CV_e$		0.47	0.59	0.43	1.45	1.24	0.80

\*\* , \* , ns: significant at 1%, 5% and not significant by the test of F. DF: degrees of freedom; FLOW: flowering; PH: plant height; FBY: fresh biomass production; EXT: juice extraction; TSS: total soluble solids; and TBH: tons of brix per hectare;  $h^2$ : heritability;  $CV_e$ : residual coefficient of variation;  $CV_g$ : coefficient of genetic variation.

For FLOW, three groups were formed, with the highest number of hybrids being observed. For PH, there were three groups, and the hybrids 201550B001, 201550B002, 201550B004, 201550B005 and 201550B019 stood out. For FBY, there were five groups, highlighting the 201555B004, 201550B010, 201550B019, 201550B025 and 201550B026 hybrids. For EXT, there were five groups formed, and the hybrids that stood out were 201550B007, 201550B014, 201550B015, 201550B022, and 20150B025. For the TSS, four groups were formed, but for this variable, the hybrids 201550B024 and 201550B026 were superior to all the evaluated controls. And for TBH, three groups were formed, showing that the hybrids 201550B025, 201550B026, and 201550B028 were also superior to all the controls.

To evaluate the genetic gain, selection intensity of approximately 10% (4 individuals) was used (Table 4). In relation to the FLOW, the best genetic gain was 0.74% through the selection index MM, with equal weight for  $CV_g/CV_e$  and  $SD$ .

Table 3. Means of 36 sweet sorghum genotypes evaluated in Sete Lagoas and Nova Porteirinha.

	<i>FLOW</i>		<i>PH</i>		<i>FBY</i>		<i>EXT</i>		<i>TSS</i>		<i>TBH</i>
CMSXS643	84.67 <sup>a</sup>	CV568	3.60 <sup>a</sup>	201550B026	72.59 <sup>a</sup>	CMSXS647	49.50 <sup>a</sup>	201550B026	19.87 <sup>a</sup>	201550B025	14.65 <sup>a</sup>
CV568	84.00 <sup>a</sup>	CV198	3.59 <sup>a</sup>	201550B025	72.14 <sup>a</sup>	201550B015	49.14 <sup>a</sup>	201550B024	19.87 <sup>a</sup>	201550B026	13.49 <sup>a</sup>
CV198	83.83 <sup>a</sup>	201550B004	3.42 <sup>b</sup>	CV568	71.92 <sup>a</sup>	201550B014	48.38 <sup>a</sup>	BRS 508	19.85 <sup>a</sup>	201550B028	13.38 <sup>a</sup>
BRS 508	81.67 <sup>b</sup>	201550B005	3.35 <sup>b</sup>	201550B010	71.04 <sup>a</sup>	201550B007	48.22 <sup>a</sup>	201550B028	19.85 <sup>a</sup>	CV198	13.19 <sup>a</sup>
CMSXS630	78.17 <sup>b</sup>	201550B001	3.31 <sup>b</sup>	201550B019	69.42 <sup>a</sup>	BRS 511	48.10 <sup>a</sup>	201550B002	19.60 <sup>a</sup>	CV568	12.92 <sup>a</sup>
201550B004	76.83 <sup>b</sup>	201550B019	3.29 <sup>b</sup>	201550B004	68.08 <sup>b</sup>	CMSXS646	48.04 <sup>a</sup>	201550B005	19.52 <sup>a</sup>	201550B004	12.77 <sup>a</sup>
BRS 511	76.5 <sup>b</sup>	201550B002	3.29 <sup>b</sup>	201550B011	68.02 <sup>b</sup>	201550B022	47.85	CMSXS643	19.50 <sup>a</sup>	201550B022	12.70 <sup>a</sup>
201550B009	76.33 <sup>b</sup>	201550B027	3.28 <sup>b</sup>	201550B009	67.14 <sup>b</sup>	201550B025	47.5 <sup>a</sup>	BRS 511	19.47 <sup>a</sup>	201550B002	12.62 <sup>a</sup>
201550B026	76.17 <sup>b</sup>	201550B022	3.25 <sup>b</sup>	201550B008	66.66 <sup>b</sup>	201550B017	47.2 <sup>a</sup>	201550B003	19.45 <sup>a</sup>	201550B019	12.62 <sup>a</sup>
CMSXS647	76.17 <sup>b</sup>	201550B011	3.25 <sup>b</sup>	201550B028	66.22 <sup>b</sup>	201550B011	46.85 <sup>b</sup>	201550B027	19.43 <sup>a</sup>	201550B009	12.24 <sup>a</sup>
201550B028	75.50 <sup>b</sup>	201550B026	3.24 <sup>b</sup>	201550B022	65.38 <sup>c</sup>	CV198	46.46 <sup>b</sup>	CMSXS646	19.27 <sup>a</sup>	201550B011	12.14 <sup>a</sup>
201550B020	75.50 <sup>b</sup>	201550B025	3.23 <sup>b</sup>	CMSXS643	65.14 <sup>c</sup>	201550B008	46.32 <sup>b</sup>	201550B020	19.27 <sup>a</sup>	CMSXS630	12.02 <sup>a</sup>
201550B027	74.83 <sup>b</sup>	BRS 508	3.18 <sup>c</sup>	201550B002	65.12 <sup>c</sup>	201550B024	46.02 <sup>b</sup>	201550B025	19.18 <sup>a</sup>	CMSXS643	12.01 <sup>a</sup>
201550B005	74.83 <sup>b</sup>	201550B024	3.17 <sup>c</sup>	CV198	64.5 <sup>c</sup>	201550B006	45.94 <sup>b</sup>	201550B018	19.12 <sup>a</sup>	201550B017	11.91 <sup>a</sup>
201550B010	74.67 <sup>b</sup>	CMSXS643	3.13 <sup>c</sup>	201550B016	64.17 <sup>c</sup>	201550B013	45.92 <sup>b</sup>	201550B010	19.08 <sup>a</sup>	201550B023	11.83 <sup>a</sup>
CMSXS646	74.33 <sup>b</sup>	CMSXS630	3.13 <sup>c</sup>	201550B017	64.00 <sup>c</sup>	201550B019	45.40 <sup>b</sup>	201550B004	19.08 <sup>a</sup>	201550B010	11.73 <sup>a</sup>
201550B001	74.33 <sup>b</sup>	201550B028	3.11 <sup>c</sup>	CMSXS630	63.90 <sup>c</sup>	201550B012	45.40 <sup>b</sup>	201550B009	19.07 <sup>a</sup>	201550B008	11.63 <sup>a</sup>
201550B019	74.19 <sup>b</sup>	201550B020	3.11 <sup>c</sup>	201550B020	63.59 <sup>c</sup>	201550B003	45.34 <sup>b</sup>	201550B011	18.97 <sup>a</sup>	201550B020	11.31 <sup>a</sup>
201550B015	73.67 <sup>b</sup>	BRS 511	3.08 <sup>c</sup>	201550B006	63.13 <sup>c</sup>	201550B005	45.33 <sup>b</sup>	201550B022	18.88 <sup>b</sup>	BRS 508	11.21 <sup>a</sup>
201550B018	73.17 <sup>b</sup>	CMSXS646	3.08 <sup>c</sup>	201550B001	62.95 <sup>c</sup>	CV568	45.16 <sup>b</sup>	201550B001	18.85 <sup>b</sup>	CMSXS647	11.18 <sup>b</sup>
201550B013	73.17 <sup>b</sup>	201550B010	3.06 <sup>c</sup>	201550B023	62.77 <sup>c</sup>	201550B002	44.87 <sup>c</sup>	201550B019	18.73 <sup>b</sup>	201550B006	11.11 <sup>b</sup>
201550B017	73.00 <sup>c</sup>	201550B017	3.06 <sup>c</sup>	201550B021	60.95 <sup>d</sup>	201550B028	44.36 <sup>c</sup>	CMSXS630	18.67 <sup>b</sup>	201550B015	11.06 <sup>b</sup>

Continue

Table 3. Means of 36 sweet sorghum genotypes evaluated in Sete Lagoas and Nova Porteirinha.

	<i>FLOW</i>		<i>PH</i>		<i>FBY</i>		<i>EXT</i>		<i>TSS</i>		<i>TBH</i>
201550B014	72.50 <sup>c</sup>	201550B021	3.06 <sup>c</sup>	201550B012	60.47 <sup>d</sup>	201550B010	44.31 <sup>c</sup>	201550B008	18.67 <sup>b</sup>	BRS 511	10.87 <sup>b</sup>
201550B025	72.17 <sup>c</sup>	201550B018	3.06 <sup>c</sup>	201550B005	60.18 <sup>d</sup>	201550B001	43.69 <sup>c</sup>	CV198	18.52 <sup>b</sup>	201550B001	10.68 <sup>b</sup>
201550B022	71.67 <sup>c</sup>	201550B014	3.05 <sup>c</sup>	201550B015	58.37 <sup>d</sup>	201550B027	43.63 <sup>c</sup>	201550B023	18.35 <sup>b</sup>	201550B024	10.61 <sup>b</sup>
201550B003	71.67 <sup>c</sup>	201550B016	3.05 <sup>c</sup>	201550B014	58.04 <sup>d</sup>	201550B016	43.33 <sup>c</sup>	201550B021	18.25 <sup>b</sup>	201550B027	10.47 <sup>b</sup>
201550B023	71.33 <sup>c</sup>	201550B003	3.03 <sup>c</sup>	CMSXS646	57.22 <sup>d</sup>	201550B026	43.30 <sup>c</sup>	CMSXS647	18.13 <sup>b</sup>	201550B016	10.25 <sup>b</sup>
201550B008	71.33 <sup>c</sup>	201550B008	3.03 <sup>c</sup>	201550B027	55.23 <sup>d</sup>	201550B021	42.88 <sup>c</sup>	201550B017	18.05 <sup>c</sup>	CMSXS646	10.23 <sup>b</sup>
201550B024	71.17 <sup>c</sup>	201550B006	3.02 <sup>c</sup>	201550B013	54.50 <sup>d</sup>	201550B004	42.45 <sup>c</sup>	201550B006	17.93 <sup>c</sup>	201550B014	10.19 <sup>b</sup>
201550B021	70.83 <sup>c</sup>	201550B009	2.96 <sup>c</sup>	CMSXS647	54.00 <sup>e</sup>	201550B009	41.67 <sup>d</sup>	201550B015	17.62 <sup>c</sup>	201550B003	10.06 <sup>b</sup>
201550B002	70.83 <sup>c</sup>	201550B013	2.96 <sup>c</sup>	201550B024	53.94 <sup>e</sup>	201550B023	41.67 <sup>d</sup>	201550B007	17.35 <sup>c</sup>	201550B005	9.65 <sup>c</sup>
201550B012	70.00 <sup>c</sup>	201550B015	2.96 <sup>c</sup>	201550B007	52.43 <sup>e</sup>	CMSXS630	41.55 <sup>d</sup>	201550B014	17.25 <sup>c</sup>	201550B021	9.62 <sup>c</sup>
201550B007	70.00 <sup>c</sup>	201550B023	2.95 <sup>c</sup>	201550B018	50.51 <sup>e</sup>	201550B020	41.17 <sup>d</sup>	201550B016	16.87 <sup>c</sup>	201550B018	9.23 <sup>c</sup>
201550B006	69.83 <sup>c</sup>	201550B012	2.93 <sup>c</sup>	201550B003	49.96 <sup>e</sup>	CMSXS643	40.65 <sup>d</sup>	CV568	15.92 <sup>d</sup>	201550B012	9.01 <sup>c</sup>
201550B016	69.67 <sup>c</sup>	201550B007	2.87 <sup>c</sup>	BRS 508	47.91 <sup>e</sup>	BRS 508	40.35 <sup>d</sup>	201550B012	15.52 <sup>d</sup>	201550B007	9.00 <sup>c</sup>
201550B011	69.17 <sup>c</sup>	CMSXS647	2.79 <sup>c</sup>	BRS 511	45.63 <sup>e</sup>	201550B018	38.15 <sup>e</sup>	201550B013	14.63 <sup>d</sup>	201550B013	7.73 <sup>c</sup>

Means followed by equal letters do not differ from one another by the Scott-Knott test, at 5% probability. *FLOW*: flowering; *PH*: plant height; *FBY*: fresh biomass production; *EXT*: juice extraction; *TSS*: total soluble solids; and *TBH*: tons of brix per hectare



Table 4. Estimates of selection gain (SG) based on the selection differential, for all the traits evaluated among the 36 sweet sorghum genotypes, in Sete Lagoas and Nova Porteirinha.

Indexes	Weight	SG %					
		FLOW	PH	FBY	EXT	TSS	TBH
W	PA	-0.50	1.20	0.07	0.84	3.05	4.93
	$CV_g$	-0.56	1.23	0.06	2.42	1.48	4.42
	$CV_g/CV_e$	-0.45	1.10	0.07	1.68	2.44	4.98
	SD	-0.72	0.55	0.06	2.57	1.43	3.78
MM	PA	-0.32	1.20	0.08	1.14	2.32	4.93
	$CV_g$	-0.15	0.84	0.06	0.06	3.79	5.73
	$CV_g/CV_e$	-0.74	1.23	0.05	2.12	2.21	4.42
	SD	-0.74	1.23	0.05	2.12	2.21	4.42

FLOW: flowering; PH: plant height; FBY: fresh biomass production; EXT: juice extraction; TSS: total soluble solids; and TBH: tons of brix per hectare. W: Williams Index; MM: Mulamba & Mock Index; PA: attributed weight per attempts (1.5, 1.3 and 1.1);  $CV_g$ : coefficient of genetic variation;  $CV_e$ : residual coefficient of variation; SD: standard deviation.

This result was interesting for the trait flowering, since it indicates that the cycle of the crop will be shorter, once the accumulation of soluble solids occurs after the flowering, presenting earlier good quality genotypes for juice. In relation to PH, the highest gain was obtained through the W and MM index (1.23%), with weight equal to  $CV_g$  for the W index and weight equal to  $CV_g/CV_e$  and SD for MM. For the FBY, the highest genetic gain observed was 0.08%, through the MM index, with an attributed weight per attempts (PA). In relation to EXT, the highest genetic gain observed was 2.57% for W index, with weight equal to SD. For TSS, the highest gain was 3.79% through the MM index, with weight equal to  $CV_g$ . And for TBH, the highest gain observed was 5.73%, with the MM index, with weight equal to  $CV_g$ . In general, it was possible to observe variations between the two indexes studied with the different economic weights and parameters (Table 4). However, the Mulamba & Mock index was more favorable for hybrid selection than the Williams index. França et al., 2016 compared different selection indexes applied to multiple agronomic traits in sweet sorghum and found that significant genetic gains of agronomic traits can be observed through the use of this simultaneous selection (Leite et al., 2017; Krause et al., 2012).

The selected hybrids for each selection index, and their respective weight, are represented in table 5.

Table 5. Sweet sorghum hybrids selected using the selection indexes of Williams (1962) and Mulamba &amp; Mock (1978).

Indexes	Weight	Select hybrids
W	PA	201550B011, 201550B019, 201550B025, 201555B026
	$CV_g$	201550B011, 201550B019, 201550B022, 201550B025
	$CV_g/CV_e$	201550B011, 201550B022, 201550B025, 201550B026
	SD	201550B008, 201550B011, 201550B022, 201550B025
MM	PA	201550B002, 201550B011, 201550B025, 201550B026
	$CV_g$	201550B002, 201550B025, 201550B026, 201550B028
	$CV_g/CV_e$	201550B002, 201550B011, 201550B022, 201550B025
	SD	201550B002, 201550B011, 201550B022, 201550B025

W: Williams Index; MM: Mulamba & Mock Index; PA: attributed weight per attempts (1.5, 1.3 and 1.1);  $CV_g$ : coefficient of genetic variation;  $CV_e$ : residual coefficient of variation; SD: standard deviation.

The identification of the promising sweet sorghum hybrids for bioenergy production, it was observed that most of the hybrids selected through multiple comparison test coincided with the best performance hybrids identified through the selection indexes of Williams and Mulamba & Mock for the agro-industrial traits of interest that were evaluated, highlighting the hybrids 20155B0002, 201550B011, 201550B022, 201550B025, 201550B026 and 201550B028, with high potential for bioethanol production. The genotypes with the highest production potential for bioenergy showed superior performance for most of the studied traits, with the exception of flowering, in which the previous hybrids were selected (Figure 1).

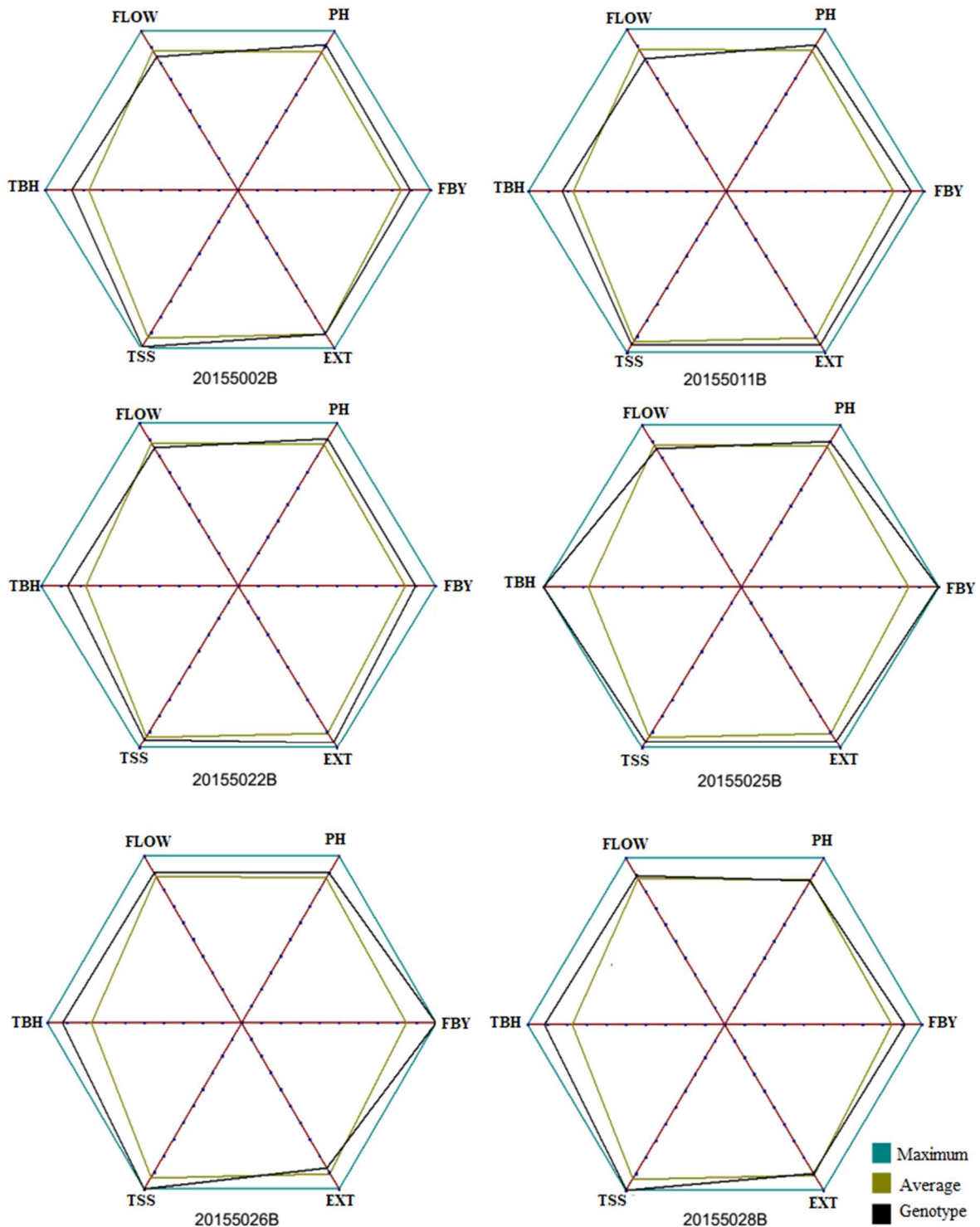


Figure 1. Graphical representation of selected hybrids for all the traits: FLOW: flowering; PH: plant height; FBY: fresh biomass production; EXT: juice extraction; TSS: total soluble solids; and TBH: tons of brix per hectare.

This result was satisfactory to optimize the genetic breeding of sweet sorghum for ethanol production, making it possible to select agronomic and industrial traits simultaneously and contributed to the selection of genotypes based on a complex set of traits.

## CONCLUSIONS

The sweet sorghum hybrids (20155B0002, 201550B011, 201550B022, 201550B025, 201550B026 and 201550B028) were identified as promising for bioenergy production considering multiple traits analysis.

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